

Daniel Shriner

List of Publications by Year in descending order

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Version: 2024-02-01

101
papers

6,677
citations

81743

39
h-index

66788

78
g-index

111
all docs

111
docs citations

111
times ranked

12969
citing authors

#	ARTICLE	IF	CITATIONS
1	Additive genetic effect of GCKR, G6PC2, and SLC30A8 variants on fasting glucose levels and risk of type 2 diabetes. PLoS ONE, 2022, 17, e0269378.	1.1	4
2	Endemic Burkitt Lymphoma in second-degree relatives in Northern Uganda: in-depth genome-wide analysis suggests clues about genetic susceptibility. Leukemia, 2021, 35, 1209-1213.	3.3	5
3	Trans-ethnic meta-analysis identifies new loci associated with longitudinal blood pressure traits. Scientific Reports, 2021, 11, 4075.	1.6	13
4	A UGT1A1 variant is associated with serum total bilirubin levels, which are causal for hypertension in African-ancestry individuals. Npj Genomic Medicine, 2021, 6, 44.	1.7	6
5	CWAS in Africans identifies novel lipids loci and demonstrates heterogenous association within Africa. Human Molecular Genetics, 2021, 30, 2205-2214.	1.4	6
6	Evolutionary genetics and acclimatization in nephrology. Nature Reviews Nephrology, 2021, 17, 827-839.	4.1	5
7	Refining genome-wide associated loci for serum uric acid in individuals with African ancestry. Human Molecular Genetics, 2020, 29, 506-514.	1.4	6
8	High-depth African genomes inform human migration and health. Nature, 2020, 586, 741-748.	13.7	197
9	Genetic modifiers of long-term survival in sickle cell anemia. Clinical and Translational Medicine, 2020, 10, e152.	1.7	21
10	Ancient familial Mediterranean fever mutations in human pyrin and resistance to Yersinia pestis. Nature Immunology, 2020, 21, 857-867.	7.0	90
11	Admixture mapping identifies genetic regions associated with blood pressure phenotypes in African Americans. PLoS ONE, 2020, 15, e0232048.	1.1	12
12	<i>HLA</i> and autoantibodies define scleroderma subtypes and risk in African and European Americans and suggest a role for molecular mimicry. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 552-562.	3.3	52
13	Time-to-event modeling of hypertension reveals the nonexistence of true controls. ELife, 2020, 9, .	2.8	1
14	Title is missing!. , 2020, 15, e0232048.		0
15	Title is missing!. , 2020, 15, e0232048.		0
16	Title is missing!. , 2020, 15, e0232048.		0
17	Title is missing!. , 2020, 15, e0232048.		0
18	ZRANB3 is an African-specific type 2 diabetes locus associated with beta-cell mass and insulin response. Nature Communications, 2019, 10, 3195.	5.8	69

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19	Type 2 diabetes complications and comorbidity in Sub-Saharan Africans. <i>EClinicalMedicine</i> , 2019, 16, 30-41.	3.2	58
20	Pharmacogenomics and Infectious Diseases in Africa. , 2019, , 95-127.		0
21	Genetics of cognitive trajectory in Brazilians: 15 years of follow-up from the BambuÃ-Epigen Cohort Study of Aging. <i>Scientific Reports</i> , 2019, 9, 18085.	1.6	6
22	Whole-Genome-Sequence-Based Haplotypes Reveal Single Origin of the Sickle Allele during the Holocene Wet Phase. <i>American Journal of Human Genetics</i> , 2018, 102, 547-556.	2.6	77
23	Genetic Ancestry of Hadza and Sandawe Peoples Reveals Ancient Population Structure in Africa. <i>Genome Biology and Evolution</i> , 2018, 10, 875-882.	1.1	6
24	Genetic history of Chad. <i>American Journal of Physical Anthropology</i> , 2018, 167, 804-812.	2.1	10
25	Brief Report: Whole-Exome Sequencing to Identify Rare Variants and Gene Networks That Increase Susceptibility to Scleroderma in African Americans. <i>Arthritis and Rheumatology</i> , 2018, 70, 1654-1660.	2.9	10
26	Re-analysis of Whole Genome Sequence Data From 279 Ancient Eurasians Reveals Substantial Ancestral Heterogeneity. <i>Frontiers in Genetics</i> , 2018, 9, 268.	1.1	5
27	Analyses of genome wide association data, cytokines, and gene expression in African-Americans with benign ethnic neutropenia. <i>PLoS ONE</i> , 2018, 13, e0194400.	1.1	36
28	Transferability of genome-wide associated loci for asthma in African Americans. <i>Journal of Asthma</i> , 2017, 54, 1-8.	0.9	11
29	Human ancestry correlates with language and reveals that race is not an objective genomic classifier. <i>Scientific Reports</i> , 2017, 7, 1572.	1.6	66
30	Genome-wide analysis identifies an african-specific variant in <i>SEMA4D</i> associated with body mass index. <i>Obesity</i> , 2017, 25, 794-800.	1.5	30
31	Overview of Admixture Mapping. <i>Current Protocols in Human Genetics</i> , 2017, 94, 1.23.1-1.23.8.	3.5	34
32	The genomic landscape of African populations in health and disease. <i>Human Molecular Genetics</i> , 2017, 26, R225-R236.	1.4	64
33	Common and rare exonic MUC5B variants associated with type 2 diabetes in Han Chinese. <i>PLoS ONE</i> , 2017, 12, e0173784.	1.1	10
34	Impact of Type 2 Diabetes on Impaired Kidney Function in Sub-Saharan African Populations. <i>Frontiers in Endocrinology</i> , 2016, 7, 50.	1.5	9
35	Migration Route Out of Africa Unresolved by 225 Egyptian and Ethiopian Whole Genome Sequences. <i>Frontiers in Genetics</i> , 2016, 7, 98.	1.1	4
36	The African diaspora: history, adaptation and health. <i>Current Opinion in Genetics and Development</i> , 2016, 41, 77-84.	1.5	44

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37	Ancient Human Migration after Out-of-Africa. <i>Scientific Reports</i> , 2016, 6, 26565.	1.6	15
38	Estimation of F_{ST} and the Impact of de novo Mutation. <i>Human Heredity</i> , 2016, 82, 37-49.	0.4	1
39	Evolutionary context for the association of $\hat{\beta}$ -globin, serum uric acid, and hypertension in African Americans. <i>BMC Medical Genetics</i> , 2015, 16, 103.	2.1	7
40	Phenotypic variance explained by local ancestry in admixed African Americans. <i>Frontiers in Genetics</i> , 2015, 6, 324.	1.1	13
41	Evaluation of Genome Wide Association Study Associated Type 2 Diabetes Susceptibility Loci in Sub Saharan Africans. <i>Frontiers in Genetics</i> , 2015, 6, 335.	1.1	50
42	An Improved Fst Estimator. <i>PLoS ONE</i> , 2015, 10, e0135368.	1.1	6
43	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462.	13.7	173
44	Genome-wide genotype and sequence-based reconstruction of the 140,000 year history of modern human ancestry. <i>Scientific Reports</i> , 2015, 4, 6055.	1.6	54
45	Mixed Ancestry and Disease Risk Transferability. <i>Current Genetic Medicine Reports</i> , 2015, 3, 151-157.	1.9	3
46	APOL1 G1 genotype modifies the association between HDLC and kidney function in African Americans. <i>BMC Genomics</i> , 2015, 16, 421.	1.2	9
47	Genome-wide association study identifies African-ancestry specific variants for metabolic syndrome. <i>Molecular Genetics and Metabolism</i> , 2015, 116, 305-313.	0.5	41
48	Gene-Based Sequencing Identifies Lipid-Influencing Variants with Ethnicity-Specific Effects in African Americans. <i>PLoS Genetics</i> , 2014, 10, e1004190.	1.5	34
49	Meta-Analysis of Genome-Wide Association Studies in African Americans Provides Insights into the Genetic Architecture of Type 2 Diabetes. <i>PLoS Genetics</i> , 2014, 10, e1004517.	1.5	191
50	Accounting for Linkage Disequilibrium in Association Analysis of Diverse Populations. <i>Genetic Epidemiology</i> , 2014, 38, 265-273.	0.6	25
51	Reconciling clinical importance and statistical significance. <i>European Journal of Human Genetics</i> , 2014, 22, 158-159.	1.4	1
52	Impact of Hardy-Weinberg disequilibrium on post-imputation quality control. <i>Human Genetics</i> , 2013, 132, 1073-1075.	1.8	7
53	Genome-wide Association Analysis of Blood-Pressure Traits in African-Ancestry Individuals Reveals Common Associated Genes in African and Non-African Populations. <i>American Journal of Human Genetics</i> , 2013, 93, 545-554.	2.6	189
54	Genome science and health disparities: a growing success story?. <i>Genome Medicine</i> , 2013, 5, 61.	3.6	14

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55	Genome-Wide Association of Body Fat Distribution in African Ancestry Populations Suggests New Loci. PLoS Genetics, 2013, 9, e1003681.	1.5	109
56	Overview of Admixture Mapping. Current Protocols in Human Genetics, 2013, 76, Unit 1.23.	3.5	76
57	Variation in <i>APOL1</i> Contributes to Ancestry-Level Differences in HDLc-Kidney Function Association. International Journal of Nephrology, 2012, 2012, 1-10.	0.7	28
58	C-reactive protein (CRP) promoter polymorphisms influence circulating CRP levels in a genome-wide association study of African Americans. Human Molecular Genetics, 2012, 21, 3063-3072.	1.4	32
59	UGT1A1 is a major locus influencing bilirubin levels in African Americans. European Journal of Human Genetics, 2012, 20, 463-468.	1.4	63
60	Genome-wide association study identifies novel loci association with fasting insulin and insulin resistance in African Americans. Human Molecular Genetics, 2012, 21, 4530-4536.	1.4	80
61	Improved Eigenanalysis of Discrete Subpopulations and Admixture Using the Minimum Average Partial Test. Human Heredity, 2012, 73, 73-83.	0.4	11
62	Transferability and Fine Mapping of genome-wide associated loci for lipids in African Americans. BMC Medical Genetics, 2012, 13, 88.	2.1	33
63	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	1.1	197
64	Moving toward System Genetics through Multiple Trait Analysis in Genome-Wide Association Studies. Frontiers in Genetics, 2012, 3, 1.	1.1	231
65	Genome-wide associated loci influencing interleukin (IL)-10, IL-1Ra, and IL-6 levels in African Americans. Immunogenetics, 2012, 64, 351-359.	1.2	31
66	Multiple Loci Associated with Renal Function in African Americans. PLoS ONE, 2012, 7, e45112.	1.1	7
67	Mapping of disease-associated variants in admixed populations. Genome Biology, 2011, 12, 223.	13.9	53
68	The Roles of IL-6, IL-10, and IL-1RA in Obesity and Insulin Resistance in African-Americans. Journal of Clinical Endocrinology and Metabolism, 2011, 96, E2018-E2022.	1.8	59
69	A genome-wide association study of serum uric acid in African Americans. BMC Medical Genomics, 2011, 4, 17.	0.7	82
70	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	13.7	1,855
71	A unified framework for multi-locus association analysis of both common and rare variants. BMC Genomics, 2011, 12, 89.	1.2	10
72	Approximate and exact tests of Hardy-Weinberg equilibrium using uncertain genotypes. Genetic Epidemiology, 2011, 35, 632-637.	0.6	12

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73	Identifying a major locus that regulates spontaneous arthritis in IL-1ra-deficient mice and analysis of potential candidates. <i>Genetical Research</i> , 2011, 93, 95-103.	0.3	12
74	Genome-wide association study for serum urate concentrations and gout among African Americans identifies genomic risk loci and a novel URAT1 loss-of-function allele. <i>Human Molecular Genetics</i> , 2011, 20, 4056-4068.	1.4	101
75	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. <i>Human Molecular Genetics</i> , 2011, 20, 2273-2284.	1.4	168
76	Joint Ancestry and Association Testing in Admixed Individuals. <i>PLoS Computational Biology</i> , 2011, 7, e1002325.	1.5	88
77	Genetic Association for Renal Traits among Participants of African Ancestry Reveals New Loci for Renal Function. <i>PLoS Genetics</i> , 2011, 7, e1002264.	1.5	109
78	Practical considerations for imputation of untyped markers in admixed populations. <i>Genetic Epidemiology</i> , 2010, 34, 258-265.	0.6	32
79	Development of admixture mapping panels for African Americans from commercial high-density SNP arrays. <i>BMC Genomics</i> , 2010, 11, 417.	1.2	15
80	Genome-wide association of anthropometric traits in African- and African-derived populations. <i>Human Molecular Genetics</i> , 2010, 19, 2725-2738.	1.4	90
81	<i>FTO</i> Genetic Variation and Association With Obesity in West Africans and African Americans. <i>Diabetes</i> , 2010, 59, 1549-1554.	0.3	94
82	Circulating Adiponectin Is Associated with Obesity and Serum Lipids in West Africans. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2010, 95, 3517-3521.	1.8	37
83	Deviance information criterion (DIC) in Bayesian multiple QTL mapping. <i>Computational Statistics and Data Analysis</i> , 2009, 53, 1850-1860.	0.7	22
84	Mapping multiple quantitative trait loci under Bayes error control. <i>Genetical Research</i> , 2009, 91, 147-159.	0.3	1
85	Transferability and Fine-Mapping of Genome-Wide Associated Loci for Adult Height across Human Populations. <i>PLoS ONE</i> , 2009, 4, e8398.	1.1	47
86	Commonality of functional annotation: a method for prioritization of candidate genes from genome-wide linkage studies. <i>Nucleic Acids Research</i> , 2008, 36, e26-e26.	6.5	24
87	Putting Materials and Methods in Their Place. <i>Science</i> , 2008, 322, 1463-1463.	6.0	0
88	Detection of Gene-Gene Interactions in Genome-Wide Association Studies of Human Population Data. <i>Human Heredity</i> , 2007, 63, 67-84.	0.4	164
89	An Efficient Bayesian Model Selection Approach for Interacting Quantitative Trait Loci Models With Many Effects. <i>Genetics</i> , 2007, 176, 1865-1877.	1.2	73
90	R/qtlbim: QTL with Bayesian Interval Mapping in experimental crosses. <i>Bioinformatics</i> , 2007, 23, 641-643.	1.8	115

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91	Statistical Methods for Multiple QTL Mapping in Experimental Crosses. , 2007, , 285-323.		0
92	EVOLUTION OF INTRAHOST HIV - 1 GENETIC DIVERSITY DURING CHRONIC INFECTION. Evolution; International Journal of Organic Evolution, 2006, 60, 1165-1176.	1.1	28
93	EVOLUTION OF INTRAHOST HIV-1 GENETIC DIVERSITY DURING CHRONIC INFECTION. Evolution; International Journal of Organic Evolution, 2006, 60, 1165.	1.1	15
94	Selection on the Human Immunodeficiency Virus Type 1 Proteome following Primary Infection. Journal of Virology, 2006, 80, 9519-9529.	1.5	118
95	Evolution of intrahost HIV-1 genetic diversity during chronic infection. Evolution; International Journal of Organic Evolution, 2006, 60, 1165-76.	1.1	30
96	Influence of Random Genetic Drift on Human Immunodeficiency Virus Type 1 env Evolution During Chronic Infection. Genetics, 2004, 166, 1155-1164.	1.2	65
97	Pervasive Genomic Recombination of HIV-1 in Vivo Sequence data from this article have been deposited with the EMBL/GenBank Data Libraries under accession nos. AY496645, AY496646, AY496647, AY496648, AY496649, AY496650, AY496651, AY496652, AY496653, AY496654, AY496655, AY496656, AY496657, AY496658, AY496659, AY496660, AY496661, AY496662, AY496663, AY496664, AY496665, AY496666, AY496667, AY496668, AY496669, AY496670, AY496671, AY496672, AY496673, AY496674, AY496675, AY496676, AY496677, AY496678, AY496679, AY49. Genetics, 2004, 167, 1573-1583.	1.2	139
98	Molecular clock-like evolution of human immunodeficiency virus type 1. Virology, 2004, 329, 101-108.	1.1	15
99	Importance and detection of virus reservoirs and compartments of HIV infection. Current Opinion in Microbiology, 2003, 6, 410-416.	2.3	46
100	Evolutionary Indicators of Human Immunodeficiency Virus Type 1 Reservoirs and Compartments. Journal of Virology, 2003, 77, 5540-5546.	1.5	97
101	Potential impact of recombination on sitewise approaches for detecting positive natural selection. Genetical Research, 2003, 81, 115-121.	0.3	158